

region which is frequently involved in amplification-associated rearrangements. The nucleotide sequence reveals a mosaic organization of four Alu-equivalent repeats of the B1 and B2 families and eight long A + T-rich DNA segments. Part of this region is enriched with long imperfect **palindromes**. The center of one **palindrome** contains a putative **topoisomerase I** cleavage site and this site defines the position of a novel junction which was formed by illegitimate recombination with anther A + T-rich DNA sequence located far apart on the amplified DNA. These findings and their significance are discussed in the context of related data from other systems and in the light of current models for eukaryotic DNA recombination, replication and organization.

Record Date Created: 19871202

3/7/83 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04750214 84069794 PMID: 6316268

A site and strand specific nuclease activity with analogies to **topoisomerase I** frames the rRNA gene of Tetrahymena.

Gocke E; Bonven BJ; Westergaard O

Nucleic acids research (ENGLAND) Nov 25 1983, 11 (22) p7661-78,
ISSN 0305-1048 Journal Code: O8L

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Exposure of macronuclear chromatin from Tetrahymena thermophila to sodium dodecyl sulfate causes an endogenous nuclease to cleave the extra-chromosomal rDNA at specific sites. All cuts are single-strand cleavages specific to the non-coding strand. Three cleavages map in the central non-transcribed spacer of the **palindromic** molecule at positions -1000, -600 and -150 bp with respect to the transcription initiation point. A fourth site is located close to the transcription termination point, while no cleavage is observed in the coding region. The position of each cleavage is in the immediate neighbourhood of DNase I hypersensitive sites. Additionally, certain DNA sequence motifs are repeated in the region around the cleavages. Upon cleavage induction a protein becomes attached to the rDNA. Our results indicate covalent binding to the generated 3' end, in analogy to the aborted reaction of **topoisomerase I**.

Record Date Created: 19840126

?

09050909 PASCAL No.: 90-0219239

Tandem chromosomal duplications: role of REP sequences in the recombination event at the join-point

VENKATAKRISHNA SHYAMALA; SCHNEIDER E; FERRO-LUZZI AMES G

Univ. California, div. biochemistry molecular biology, Berkeley CA 94720, USA

Journal: EMBO journal, 1990, 9 (3) 939-946

ISSN: 0261-4189 CODEN: EMJODG Availability: INIST-19284; 354000006746980420

No. of Refs.: 48 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: United Kingdom

Language: English

We show that a family of prokaryotic repetitive sequences, called REP (repetitive extragenic **palindromic**), is involved in the formation of chromosomal rearrangements such as duplications. The join-points of seven RecA SUP + tandem duplications previously characterized in *Salmonella typhimurium*, that fuse the *hisD* gene to distant foreign promoters, were cloned and sequenced. In all seven cases they are shown to have originated by recombination between distant REP sequences. Possible roles for the known interaction between DNA **gyrase** and REP in chromosomal rearrangements are discussed

3/7/80 (Item 3 from file: 144)

DIALOG(R) File 144:Pascal

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04778069 PASCAL No.: 83-0018863

DNA cruciform structures: implications for telomere replication in eukaryotes and instability of long **palindromic** DNA sequences in prokaryotes

MCFADDEN G; MORGAN A R

Univ. Alberta, dep. biochim., Edmonton AB T6G 2H7, Canada

Journal: J. Theor. Biol., 1982, 97 (2) 343-349

ISSN: 0022-5193 Availability: CNRS-1643

No. of Refs.: 22 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: United Kingdom

Language: English

3/7/82 (Item 2 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

06332224 88029333 PMID: 3665882

A hotspot for novel amplification joints in a mosaic of Alu-like repeats and **palindromic** A + T-rich DNA.

Hyrien O; Debatisse M; Buttin G; de Saint Vincent BR

Unite de Genetique Somatique (UA CNRS 361), Institut Pasteur, Paris, France.

EMBO journal (ENGLAND) Aug 1987, 6 (8) p2401-8, ISSN 0261-4189

Journal Code: EMB

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

We have identified, in the amplified domain of adenylate deaminase (AMPD) overproducing Chinese hamster fibroblasts, a 2.6 kb recombinogenic DNA

3/7/3 (Item 3 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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11962205 BIOSIS NO.: 199900208314

Shope fibroma virus DNA **topoisomerase** catalyses Holliday junction resolution and hairpin formation in vitro.

AUTHOR: Palaniyar Nades; Gerasimopoulos Efthalia; Evans David H(a)

AUTHOR ADDRESS: (a) Department of Molecular Biology and Genetics, University of Guelph, Guelph, ON, N1G 2W1**Canada

JOURNAL: Journal of Molecular Biology 287 (1):p9-20 March 19, 1999

ISSN: 0022-2836

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: The telomeres of poxviral chromosomes comprise covalently closed hairpin structures bearing mismatched bases. These hairpins are formed as concatemeric replication intermediates and are processed into mature, unit-length genomes. The structural transitions and enzymes involved in telomere resolution are poorly understood. Here we show that the type I **topoisomerase** of Shope fibroma virus (SFV) can promote a recombination reaction which converts cloned SFV replication intermediates into hairpin-ended molecules resembling mature poxviral telomeres. Recombinant SFV **topoisomerase** linearised a **palindromic** plasmid bearing 1.5 kb of DNA encoding the SFV concatemer junction, at a site near the centre of inverted-repeat symmetry. Most of these linear reaction products bore hairpin tips as judged by denaturing gel electrophoresis. The resolution reaction required **palindromic** SFV DNA sequences and was inhibited by compounds which block branch migration (MgCl₂) or poxviral topoisomerases. The resolution reaction was also slow, needed substantial quantities of **topoisomerase**, and required that the **palindrome** be extruded in a cruciform configuration. DNA cleavage experiments identified a pair of suitably oriented **topoisomerase** recognition sites, 90 bases from the centre of the cloned SFV terminal inverted repeat, which may mark the resolution site. These data suggest a resolution scheme in which branch migration of a Holliday junction through a site occupied by covalently bound **topoisomerase** molecules, could lead to telomere resolution.

3/7/4 (Item 4 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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11728883 BIOSIS NO.: 199800510614

Comparative structural analysis by (1H,31P)-NMR and restrained molecular dynamics of two DNA hairpins from a strong DNA **topoisomerase** II cleavage site.

AUTHOR: Mauffret O; Amir-Aslani A; Maroun R G; Monnot M; Lescot E; Fermandjian S(a)

AUTHOR ADDRESS: (a) Dep. Biol. Structurale Pharmacol. Mol. (CNRS UMR 1772), PR2, Inst. Gustave Roussy, 94805 Villeju**France

JOURNAL: Journal of Molecular Biology 28 (3):p643-655 Oct. 30, 1998

ISSN: 0022-2836

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The structural analysis of two single-stranded DNAs d(AGCTTATCATCGATAAGCT) (ATC-19) and d(AGCTTATCGATGATAAGCT) (GAT-19) was performed by NMR and restrained molecular dynamics. These oligonucleotides reproduce the 15-33 segment of phage pBR322 DNA, which contains a strong cleavage site for **topoisomerase** II coupled to the antitumor drugs VP-16 and ellipticine. Because of their partial **palindromic** nature, the two oligonucleotides ATC-19 and GAT-19 may fold back into stable hairpin structures, consisting of a stem of eight base-pairs and a loop of three residues. NMR assignments and conformational parameters were determined from combined 2D NOESY, COSY and 1H-31P spectra. Conformations of ATC-19 and GAT-19 hairpins were calculated using the X-PLOR 3.1 program. Structures were generated through simulated annealing procedures starting from 50 structures with randomized torsion angles. A good convergence was observed for ATC-19 molecules, while no consensus was found for GAT-19. Within the GAT-19 loop, the base stacking was poor and no hydrogen bond could be detected. In contrast, ATC-19 displayed a well-defined three residue loop stabilized by both extensive base stackings and hydrogen bonding between the N3 atom of the adenine ring and the amino group of the cytosine ring. The results confirm our earlier ATC-19 structure obtained by a completely different calculation procedure (JUMNA) and the higher thermal stability of ATC-19 compared to GAT-19. Moreover, due to its mismatched basepair, the ATC-19 loop may be better described as a single residue loop rather than a three residue loop. Comparison of this loop to those containing sheared purine-purine base-pairs revealed striking resemblances, particularly on the backbone angle combination. Finally, the differences observed between the ATC-19 and GAT-19 structures could help toward understanding the sequential cleavage of DNA strands by **topoisomerase** II.

3/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11250932 BIOSIS NO.: 199800032264

In vivo cleavage of Escherichia coli BIME-2 repeats by DNA **gyrase**:

Genetic characterization of the target and identification of the cut site.

AUTHOR: Espeli Olivier; Boccard Frederic(a)

AUTHOR ADDRESS: (a)Cent. Genet. Mol. CNRS, UPR 9061, Bat. 26, Av. de la Terrasse, 91198 Gif-sur-Yvette Cedex**France

JOURNAL: Molecular Microbiology 26 (4):p767-777 Nov., 1997

ISSN: 0950-382X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The Escherichia coli chromosome contains about 300 bacterial interspersed mosaic elements (BIMes). These elements, located at the 3' end of genes, are composed of three types of alternating repetitive extragenic **palindromes** (REPs). Based on the type of REP they contain and on their ability to interact with the integration host factor (IHF), BIMes are subdivided into two families: BIME-1 elements contain an

IHF binding site flanked by converging Y and Z1 REPs, whereas BIME-2 elements contain a variable number of alternating Y and Z2 REPs without an IHF site. Although some BIMEs have been implicated in the protection of mRNA against 3' exonucleolytic degradation, the main role of elements belonging to both families remains to be elucidated. In this paper, we used oxolinic acid, a drug that reveals potential sites of DNA **gyrase** action, to demonstrate that DNA **gyrase** interacts in vivo with BIME-2 elements. The frequency of cleavage varied from one element to another, and the cleavage pattern observed in elements containing several REPs indicated that DNA **gyrase** cut DNA every two REPs. A single cleavage site has been identified in the Y REP in six out of seven instances, and the nucleotide sequence of a 44 bp fragment containing the scission point displayed conserved residues at six positions. The lack of one of the conserved residues accounted for the absence of cleavage in most of the Z2 REPs. Our results also showed that cleaved REPs were always associated with another REP, suggesting that a pair of diverging REPs constitutes the target of DNA **gyrase**. DNA **gyrase** cleavage at repetitive BIME-2 elements may have consequences for DNA topology and genomic rearrangements.

3/7/7 (Item 7 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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10943846 BIOSIS NO.: 199799564991
The RIB element in the goaG-pspF intergenic region of Escherichia coli.
AUTHOR: Jovanovic Goran; Model Peter(a)
AUTHOR ADDRESS: (a) Lab. Genetics, Rockefeller Univ., 1230 York Ave., New York, NY 10021**USA
JOURNAL: Journal of Bacteriology 179 (10):p3095-3102 1997
ISSN: 0021-9193
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The sequence (2,700 hp) between the aldH and pspF genes of Escherichia coli was determined. The pspF gene encodes a sigma-54 transcriptional activator of the phage shock protein (psp) operon (pspA to pspE). Downstream of the pspF transcribed region are two open reading frames (ORFs), ordL and goaG, convergently oriented with respect to pspF. These two ORFs, together with the adjacent aldH gene, may constitute a novel operon (aldH-ordL-goag). The goaG-pspF intergenic region contains a complex extragenic mosaic element, RIB. The structure of this RIB element, which belongs to the BIME-1 family, is Y(REP1) gt 16 lt Z-1(REP2), where Y and Z-1 are **palindromic** units and the central 16 bases contain an L motif with an ihf consensus sequence. DNA fragments containing the L motif of the psp RIB element effectively bind integration host factor (IHF), while the Y **palindromic** unit (REP1) of the same RIB element binds DNA **gyrase** weakly. Computer prediction of the pspF mRNA secondary structure suggested that the transcribed stem-loop structures formed by the 3'-flanking region of the pspF transcript containing the RIB element can stabilize and protect pspF mRNA. Analysis of pspF steady-state mRNA levels showed that transcripts with an intact RIB element are much more abundant than those truncated at the 3' end by deletion of either the entire RIB element or a single Z-1 sequence (REP2). Thus, the pspF 3'-flanking region containing the RIB element has an important role in the stabilization of the pspF transcript.

3/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10563677 BIOSIS NO.: 199699184822
A test of the double-strand break repair model for meiotic recombination in *Saccharomyces cerevisiae*.
AUTHOR: Gilbertson Larry A(a); Stahl Franklin W
AUTHOR ADDRESS: (a)Monsanto Co., AA2G, 700 Chesterfield Village Pkwy.,
Chesterfield, MO 63198**USA
JOURNAL: Genetics 144 (1):p27-41 1996
ISSN: 0016-6731
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We tested predictions of the double-strand break repair (DSBR) model for meiotic recombination by examining the segregation patterns of small **palindromic** insertions, which frequently escape mismatch repair when in heteroduplex DNA. The **palindromes** flanked a well characterized DSB site at the ARG4 locus. The "canonical" DSBR model, in which only 5' ends are degraded and resolution of the four-stranded intermediate is by Holliday junction resolvase, predicts that hDNA will frequently occur on both participating chromatids in a single event. Tetrads reflecting this configuration of hDNA were rare. In addition, a class of tetrads not predicted by the canonical DSBR model was identified. This class represented events that produced hDNA in a "trans" configuration, on opposite strands of the same duplex on the two sides of the DSB site. Whereas most classes of convertant tetrads had typical frequencies of associated crossovers, tetrads with trans hDNA were parental for flanking markers. Modified versions of the DSBR model, including one that uses a **topoisomerase** to resolve the canonical DSBR intermediate, are supported by these data.

3/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09683672 BIOSIS NO.: 199598138590
Two Enhancer Elements for DNA Replication of pSC101, par and a **Palindromic** Binding Sequence of the Rep Protein.
AUTHOR: Ohkubo Shichi; Yamaguchi Kazuo(a)
AUTHOR ADDRESS: (a)Inst. Gen Res., Kanazawa Univ., Kanazawa 920**Japan
JOURNAL: Journal of Bacteriology 177 (3):p558-565 1995
ISSN: 0021-9193
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The minimal replication origin (ori) of the Plasmid pSC101 has been previously defined as an approx 220-bp region by using plasmids defective in the par region, which is a cis-acting determinant of plasmid stability. This ori region contains the DnaA binding sequence, three repeated sequences (iterons), and an inverted repeat (IR) element (IR-1), one of the binding sites of an initiator protein, Rep (or RepA). In the

present study, we show that plasmids containing par can replicate at a nearly normal copy number in the absence of IR-1 but still require a region (the downstream region) between the third iteron and IR-1. Because par is dispensable in plasmids retaining IR-1, par and IR-1 can compensate each other for efficient replication. The region from the DnaA box to the downstream region can support DNA replication at a reduced frequency, and it is designated "core-ori." Addition of either IR-1 or par to core-ori increases the copy number of the plasmid up to a nearly normal level. However, the IR-1 element must be located downstream of the third iteron (or upstream of the rep gene) to enhance replication of the plasmid, while the par region, to which DNA **gyrase** can bind, functions optimally regardless of its location. Furthermore, the enhancer activity of IR-1 is dependent on the helical phase of the DNA double helix, suggesting that the Rep protein bound to IR-1 stimulates the activation of ori via its interaction with another factor or factors capable of binding to individual loci within ori.

3/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09080441 BIOSIS NO.: 199497088811
Specific interaction of IHF with RIBs, a class of bacterial repetitive DNA elements located at the 3' end of transcription units.
AUTHOR: Boccard Frederic; Prentki Pierre
AUTHOR ADDRESS: Dep. Molecular Biology, Univ. Geneva, 1211 Geneva 4**
Switzerland
JOURNAL: EMBO (European Molecular Biology Organization) Journal 12 (13):p 5019-5027 1993
ISSN: 0261-4189
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The prokaryotic REP (repetitive extragenic **palindromes**) or PU (**palindromic** units) sequences are often associated with other repetitive elements, forming arrangements which have been called 'BIMES' (bacterial interspersed mosaic elements). It is estimated that the *Escherichia coli* chromosome carries approx 300 - 500 BIMES, whose biological role is at present unknown. We have identified a family of BIMES consisting of two converging REP sequences flanking a 35 bp conserved segment which carries a static DNA bend and a binding site for IHF, the integration host factor of *E. coli*. We estimate that the *E. coli* genome harbors approx 100 copies of this module, which we name 'RIB' (reiterative ihf BIME). We have analyzed by gel retardation and by footprinting the in vitro interaction of IHF with individual RIBs, and shown that the protein binds strongly and specifically to their center. We have also demonstrated binding of IHF to the chromosomal population of RIBs, using a new approach which combines two-dimensional bandshift and Southern blotting. RIB elements are at the end of transcription units, and thus define a new class of ihf sites. Possible implications for genome structure and DNA topology are discussed.

3/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07996500 BIOSIS NO.: 000093052173
MOLECULAR ANALYSIS OF THE RECOMBINATION JUNCTIONS OF LAMBDA-BIO TRANSDUCING
PHAGES
AUTHOR: KUMAGAI M; IKEDA H
AUTHOR ADDRESS: DEP. MOLECULAR BIOL., INST. MEDICAL SCI., UNIVERSITY TOKYO,
MINATO-KU, TOKYO 108, JAPAN.
JOURNAL: MOL GEN GENET 230 (1-2). 1991. 60-64. 1991
FULL JOURNAL NAME: Molecular & General Genetics
CODEN: MGGEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: To examine the mechanism of recombination involved in the
formation of specialized transducing phage during the induction of
bacteriophage .lambda., we have determined the nucleotide sequences of
the recombination junctions of .lambda.bio phages. The results indicate
that abnormal excision takes place at many sites on both bacterial and
phage genomes and that the recombination sites have short regions of
homology (5-14 bp). Some of the sequences of the recombination sites were
similar to the consensus sequences of DNA **gyrase**-cleavage sites and
repetitive extragenic **palindromic** (REP) sequences. These results
showed that abnormal excision is a type of illegitimate recombination.
The possible involvement of DNA **gyrase** in this recombination is
discussed.

3/7/21 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07043727 BIOSIS NO.: 000038116469
THE FAMILY OF REPETITIVE EXTRAGENIC **PALINDROMIC** SEQUENCES INTERACTION
WITH DNA **GYRASE** AND HISTONE-LIKE PROTEIN HU
AUTHOR: YANG Y; AMES G F-L
AUTHOR ADDRESS: DEP. BIOCHEM., UNIV. CALIF., BERKELEY, CALIF. 94720.
JOURNAL: DRLICA, R. AND M. RILEY (ED.). THE BACTERIAL CHROMOSOME. XV+469P.
AMERICAN SOCIETY OF MICROBIOLOGY: WASHINGTON, D.C., USA. ILLUS. ISBN
1-55581-018-7. 0 (0). 1990. 211-226. 1990
CODEN: 29650
RECORD TYPE: Citation
LANGUAGE: ENGLISH

3/7/23 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06605174 BIOSIS NO.: 000087047336
DNA **GYRASE** BINDS TO THE FAMILY OF PROKARYOTIC REPETITIVE EXTRAGENIC
PALINDROMIC SEQUENCES
AUTHOR: YANG Y; AMES G F-L
AUTHOR ADDRESS: DEP. BIOCHEM., UNIV. CALIF., BERKELEY, CALIF. 94720.
JOURNAL: PROC NATL ACAD SCI U S A 85 (23). 1988. 8850-8854. 1988
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: A family of repetitive extragenic **palindromic** (REP) sequences is composed of hundred of copies distributed throughout the chromosome. Their **palindromic** nature and conservation suggested that they are specifically recognized by a protein(s). We have identified DNA **gyrase** [DNA **topoisomerase** (ATP-hydrolysing), EC 5.99.1.3] as one of the REP-binding proteins. **Gyrase** has at least a 10-fold higher affinity for DNA containing REP sequences than for DNA not containing REP sequences. Binding effectiveness correlates directly with the number of REP sequences in the DNA. DNase I footprinting shows that **gyrase** protects 205 base pairs on a REP-containing DNA fragment enclosing the REP sequences. In agreement with the above results, a comparison of the REP consensus sequence with the sequence of previously identified pBR322 "strong" **gyrase** cleavage sites reveals a high degree of homology. Because REP sequences are numerous and found throughout the genome, we suggest they have physiological functions mediated through their interaction with **gyrase**, such as being sites of action for the maintenance of DNA supercoiling. In addition, we speculate that these interactions may be of a structural nature, such as involvement in the higher-order structure of the bacterial chromosome.

3/7/24 (Item 24 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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06595189 BIOSIS NO.: 000087037351
FORMATION OF DELETION IN ESCHERICHIA-COLI BETWEEN DIRECT REPEATS LOCATED IN THE LONG INVERTED REPEATS OF A CELLULAR SLIME MOLD PLASMID PARTICIPATION OF DNA **GYRASE**
AUTHOR: SAING K M; ORII H; TANAKA Y; YANAGISAWA K; MIURA A; IKEDA H
AUTHOR ADDRESS: INST. BIOL. SCI., UNIV. TSUKUBA, TSUKUBA, IBARAKI 305, JPN.
JOURNAL: MOL GEN GENET 214 (1). 1988. 1-5. 1988
FULL JOURNAL NAME: Molecular & General Genetics
CODEN: MGGEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We constructed a recombinant plasmid containing the 2.1 kb HindIII fragment of plasmid pDG1, isolated from the cellular slime mold (Dictyostelium sp. strain GAl1) and using pAG60 as cloning vector. We found that deletions of the recombinant plasmid took place frequently in Escherichia coli wild-type cells. However, the deletion was not observed when the plasmid was introduced into a strain that was an isogenic temperature-sensitive mutant of the gyrA gene. These results suggest that E. coli DNA **gyrase** is involved in the mechanisms of the deletion formation. It was shown that the 1.0 kb deletant derived from the 2.1 kb HindIII insert was produced by elimination of a 1.1 kb region. Sequence analysis of the deletants showed that cutting and rejoining took place between two out of the six nearly perfect direct repeats [21 bp **palindromic** sequences; AAAAAA(T/C)GGC(G/C)GCC(A/G)TTTTT], located near the distal ends of the inverted repeats, preserving one copy of the repeats. These sequences consist of local short inverted repeats, where cutting and rejoining occur at one of the two regions.

3/7/25 (Item 25 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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06158784 BIOSIS NO.: 000085121936

TOPOISOMERASE I CLEAVAGE SITES IDENTIFIED AND MAPPED IN THE CHROMATIN OF DICTYOSTELIUM RIBOSOMAL RNA GENES

AUTHOR: NESS P J; KOLLER T; THOMA F

AUTHOR ADDRESS: INST. FUER ZELLBIOL., ETH-HONGGERBERG, CH-8093 ZURICH, SWITZ.

JOURNAL: J MOL BIOL 200 (1). 1988. 127-140. 1988

FULL JOURNAL NAME: Journal of Molecular Biology

CODEN: JMOBA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Sites of an endogenous activity that has the properties of a DNA **topoisomerase I** have been identified on the **palindromic** ribosomal RNA genes of the slime mould *Dictyostelium discoideum*. This was done in vitro, by treating isolated nuclei with sodium dodecyl sulphate, which denatures **topoisomerase** during its cycle of nicking, strand passing and resealing, and hence reveals the DNA cleavages. It was also done in vivo using the drug camptothecin, which is believed to stabilize the cleavable complex of **topoisomerase I** plus DNA, hence increasing the chances of cleavage when sodium dodecyl sulphate is subsequently added. The cleavages in vitro and in vivo were mapped by indirect end-labelling. Both treatments cause what appear to be strong double-stranded cleavages at 200 and 2200 base-pairs and at 17 .times. 103 base-pairs upstream from the rRNA transcription start. The cleavage at 200 base-pairs was analysed in greater detail using RNA hybridization probes specific for single DNA strands. The cleavage is in fact composed of three closely spaced nicks on each DNA strand. The DNA sequence at each of the nicks is strongly homologous across 15 base-pairs. Sodium dodecyl sulphate-induced cleavage by eukaryotic **topoisomerase I** is known to yield enzyme covalently attached to the 3' cut end of the DNA. We show that protein-linked DNA restriction fragments with their 3' ends at the cleavage sites are selectively retarded on denaturing gels, which provides strong evidence that the unusual cluster of cleavages is caused by a **topoisomerase I**. Additionally, the camptothecin results revealed cleavages not only at the specific upstream sites, but also across the transcribed region. Interestingly, the zone of camptothecin-assisted cleavage does not extend as far at the 3' end of the gene as the zone of endogenous nuclease sensitivity.

3/7/26 (Item 26 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05749319 BIOSIS NO.: 000084097726

A HOTSPOT FOR NOVEL AMPLIFICATION JOINTS IN A MOSAIC OF ALU-LIKE REPEATS AND PALINDROMIC A PLUS T-RICH DNA

AUTHOR: HYRIEN O; DEBATISSE M; BUTTIN G; DE SAINT VINCENT B R

AUTHOR ADDRESS: UNITE DE GENETIQUE SOMATIQUE, INST. PASTEUR, 25, RUE DU DR. ROUX, 75724 PARIS CEDEX, 15, FRANCE.

JOURNAL: EMBO (EUR MOL BIOL ORGAN) J 6 (8). 1987. 2401-2408. 1987

FULL JOURNAL NAME: EMBO (European Molecular Biology Organization) Journal

CODEN: EMJOD

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: We have identified, in the amplified domain of adenylate deaminase (AMPD) overproducing Chinese hamster fibroblasts, a 2.6 kb recombinogenic DNA region which is frequently involved in amplification-associated rearrangements. The nucleotide sequence reveals a mosaic organization of four Alu-equivalent repeats of the B1 and B2 families and eight long A + T-rich DNA segments. Part of this region is enriched with long imperfect **palindromes**. The center of one **palindrome** contains a putative **topoisomerase I** cleavage site and this site defines the position of a novel junction which was formed by illegitimate recombination with another A + T-rich DNA sequence located far apart on the amplified DNA. These findings and their significance are discussed in the context of related data from other systems and in the light of current models for eukaryotic DNA recombination, replication and organization.

3/7/28 (Item 28 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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03847793 BIOSIS NO.: 000075025866
CRUCIFORM STRUCTURES IN **PALINDROMIC** DNA ARE FAVORED BY DNA SUPER
COILING
AUTHOR: MIZUUCHI K; MIZUUCHI M; GELLERT M
AUTHOR ADDRESS: LAB. MOL. BIOL., NATL. INST. ARTHRITIS DIABETES DIG. KIDNEY
DIS., BETHESDA, MD. 20205, USA.
JOURNAL: J MOL BIOL 156 (2). 1982. 229-244. 1982
FULL JOURNAL NAME: Journal of Molecular Biology
CODEN: JMOBA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A totally **palindromic** circular DNA was prepared by head-to-head ligation of a restriction fragment of plasmic pBR322 DNA. When negatively supercoiled, this DNA readily converts to a cruciform structure, as seen by EM or gel electrophoresis. If the DNA is further supercoiled by DNA **gyrase** after hairpin formation has been initiated, as much as 80% of the molecular length can be extruded into hairpins. The rate of formation of the cruciform structure is strongly temperature-dependent; it is at least 5-fold slower at 25.degree. C than at 35.degree. C. The **palindromic** DNA, although it contains all the necessary genetic information, is unable to transform Escherichia coli. The intracellular formation of large cruciform structures is apparently incompatible with survival of the DNA species.

3/7/30 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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07923509 Genuine Article#: 224MU Number of References: 91
Title: **Palindromic** sequences and A plus T-rich DNA elements promote illegitimate recombination in Nicotiana tabacum
Author(s): Muller AE; Kamisugi Y; Gruneberg R; Niedenhof I; Horold RJ; Meyer P (REPRINT)
Corporate Source: UNIV LEEDS, FAC BIOL SCI, LEEDS INST PLANT BIOTECHNOL &

AGR/LEEDS LS2 9JT/W YORKSHIRE/ENGLAND/ (REPRINT); UNIV LEEDS, FAC BIOL
SCI, LEEDS INST PLANT BIOTECHNOL & AGR/LEEDS LS2 9JT/W
YORKSHIRE/ENGLAND/; MAX PLANCK GESELL, MAX DELBRUCK LAB/D-50829
COLOGNE//GERMANY/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1999, V291, N1 (AUG 6), P29-46

ISSN: 0022-2836 Publication date: 19990806

Publisher: ACADEMIC PRESS LTD, 24-28 OVAL RD, LONDON NW1 7DX, ENGLAND

Language: English Document Type: ARTICLE

Abstract: Illegitimate recombination is the prevailing molecular mechanism for the integration of recombinant DNA into the genome of most eukaryotic systems and the generation of deletions by intrachromosomal recombination. We developed a ?selectable marker system to screen for intrachromosomal illegitimate recombination events in order to assess the sequence and structure-specific requirements for illegitimate recombination in tobacco. In 12 illegitimate recombination products analysed, we found that all deletion termini localise to sites of **palindromic** structures or to A+T-rich DNA elements. All deletion termini showed microhomologies of two to six nucleotides. In three plants, the recombination products contained filler-DNA or an inversion of an endogenous segment. Our data strongly suggest that illegitimate recombination in plants is mediated by a DNA synthesis-dependent process, and that this mechanism is promoted by DNA regions that can form **palindromic** structures or facilitate DNA unwinding. (C) 1999 Academic Press.

3/7/33 (Item 5 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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07175537 Genuine Article#: 132NY Number of References: 66

Title: Comparative structural analysis by [H-1,P-31]-NMR and restrained molecular dynamics of two DNA hairpins from a strong DNA **topoisomerase** II cleavage site

Author(s): Mauffret O; AmirAslani A; Maroun RG; Monnot M; Lescot E; Fermandjian S (REPRINT)

Corporate Source: INST GUSTAVE ROUSSY,CNRS, UMR 1772, DEPT BIOL STRUCT & PHARMACOL MOL, PR2/F-94805 VILLEJUIF//FRANCE/ (REPRINT); INST GUSTAVE ROUSSY,CNRS, UMR 1772, DEPT BIOL STRUCT & PHARMACOL MOL/F-94805 VILLEJUIF//FRANCE/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1998, V283, N3 (OCT 30), P643-655

ISSN: 0022-2836 Publication date: 19981030

Publisher: ACADEMIC PRESS LTD, 24-28 OVAL RD, LONDON NW1 7DX, ENGLAND

Language: English Document Type: ARTICLE

Abstract: The structural analysis of two single-stranded DNAs d(AGCTTATCATCGATAAGCT) (ATC-19) and d(AGCTTATCGATGATAAGCT) (GAT-19) was performed by NMR and restrained molecular dynamics. These oligonucleotides reproduce the 15-33 segment of phage pBR322 DNA, which contains a strong cleavage site for **topoisomerase** II coupled to the antitumor drugs VP-16 and ellipticine. Because of their partial **palindromic** nature, the two oligonucleotides ATC-19 and GAT-19 may fold back into stable hairpin structures, consisting of a stem of eight base-pairs and a loop of three residues. NMR assignments and conformational parameters were determined from combined 2D NOESY, COSY and H-1-P-31 spectra. Conformations of ATC-19 and GAT-19 hairpins were calculated using the X-PLOR 3.1 program. Structures were generated through simulated annealing procedures starting from 50 structures with randomized torsion angles. A good convergence was observed for ATC-19

molecules, while no consensus was found for GAT-19. Within the GAT-19 loop, the base stacking was poor and no hydrogen bond could be detected. In contrast, ATC-19 displayed a well-defined three residue loop stabilized by both extensive base stackings and hydrogen bonding between the N3 atom of the adenine ring and the amino group of the cytosine ring. The results confirm our earlier ATC-19 structure obtained by a completely different calculation procedure (JUMNA) and the higher thermal stability of ATC-19 compared to GAT-19. Moreover, due to its mismatched basepair, the ATC-19 loop may be better described as a single residue loop rather than a three residue loop. Comparison of this loop to those containing sheared purine purine base-pairs revealed striking resemblances, particularly on the backbone angle combination. Finally, the differences observed between the ATC-19 and GAT-19 structures could help toward understanding the sequential cleavage of DNA strands by **topoisomerase II**. (C) 1998 Academic Press.

3/7/34 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06025186 Genuine Article#: XP995 Number of References: 45
Title: A cruciform-dumbbell model for inverted dimer formation mediated by inverted repeats
Author(s): Lin CT; Lyu YL; Liu LF (REPRINT)
Corporate Source: UNIV MED & DENT NEW JERSEY, ROBERT WOOD JOHNSON MED SCH, DEPT PHARMACOL, 675 HOES LANE/PISCATAWAY/NJ/08854 (REPRINT); UNIV MED & DENT NEW JERSEY, ROBERT WOOD JOHNSON MED SCH, DEPT PHARMACOL/PISCATAWAY/NJ/08854
Journal: NUCLEIC ACIDS RESEARCH, 1997, V25, N15 (AUG 1), P3009-3016
ISSN: 0305-1048 Publication date: 19970801
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD, ENGLAND OX2 6DP
Language: English Document Type: ARTICLE
Abstract: Small inverted repeats (small **palindromes**) on plasmids have been shown to mediate a recombinational rearrangement event in *Escherichia coli* leading to the formation of inverted dimers (giant **palindromes**). This recombinational rearrangement event is efficient and independent of RecA and RecBCD. In this report, we propose a cruciform-dumbbell model to explain the inverted dimer formation mediated by inverted repeats. In this model, the inverted repeats promote the formation of a DNA cruciform which is processed by an endonuclease into a linear DNA with two hairpin loops at its ends. Upon DNA replication, this linear dumbbell-like DNA is then converted to the inverted dimer. In support of this model, linear dumbbell DNA molecules with unidirectional origin of DNA replication (ColE1 ori) have been constructed and shown to transform *E. coli* efficiently resulting in the formation of the inverted dimer. The ability of linear dumbbell DNA to transform *E. coli* suggests that the terminal loops may be important in bypassing the requirement of DNA supercoiling for initiation of replication of the ColE1 ori.

3/7/35 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05188153 Genuine Article#: VF683 Number of References: 8

Title: ACTION OF DNA **GYRASE** AT RIP ELEMENTS IN ESCHERICHIA-COLI
Author(s): CLARKSON S; BATES AD
Corporate Source: UNIV LIVERPOOL, DEPT BIOCHEM, POB 147/LIVERPOOL L69
3BX/MERSEYSIDE/ENGLAND/
Journal: BIOCHEMICAL SOCIETY TRANSACTIONS, 1996, V24, N3 (AUG), PS420
ISSN: 0300-5127
Language: ENGLISH Document Type: ARTICLE

3/7/36 (Item 8 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04603340 Genuine Article#: TW702 Number of References: 48
Title: EVIDENCE FOR INVOLVEMENT OF ESCHERICHIA-COLI GENES PMBA, CSRA AND A
PREVIOUSLY UNRECOGNIZED GENE TLDD, IN THE CONTROL OF DNA **GYRASE**
BY LETD (CCDB) OF SEX FACTOR-F
Author(s): MURAYAMA N; SHIMIZU H; TAKIGUCHI S; BABA Y; AMINO H; HORIUCHI T;
SEKIMIZU K; MIKI T
Corporate Source: KYUSHU UNIV 62, FAC PHARMACEUT SCI, HIGASHI KU, MAIDASHI
3-1-1/FUKUOKA 812//JAPAN//; KYUSHU UNIV 62, FAC PHARMACEUT SCI, HIGASHI
KU/FUKUOKA 812//JAPAN/
Journal: JOURNAL OF MOLECULAR BIOLOGY, 1996, V256, N3 (MAR 1), P483-502
ISSN: 0022-2836
Language: ENGLISH Document Type: ARTICLE

Abstract: The letA (ccdA) and letD (ccdB) genes of the F plasmid, located just outside the sequence essential for replication, contribute to stable maintenance of the plasmid in Escherichia coli cells. The letD gene product acts to inhibit partitioning of chromosomal DNA and cell division by inhibiting DNA **gyrase** activity, whereas the letA gene product acts to reverse the inhibitory activity of the letD gene product. To identify the host factor(s) involved in this process, we analyzed the mutants that escaped letD expression and their suppressor, and found that the three E. coli genes tldD, tldE and zfiA participate in the process, in addition to the groE genes we reported previously. The tldD and tldE mutations made cells tolerant for letD expression, as did groE mutations, while the mutation in the zfiA gene made tldD, tldE and groE mutants LetD sensitive. We hypothesize that these gene products are factors that modulate activity of DNA **gyrase** along with the letD gene product; the zfiA gene product acts to inhibit interaction between the LetD protein and the A subunit of DNA **gyrase**, while the tldD, tldE and groE gene products act to suppress the inhibitory activity of the zfiA gene product. The tldD, tldE, and zfiA genes are located at 70.4, 96.0 and 58.2 minutes on the E. coli chromosome, respectively, and code for proteins with relative molecular masses of 51,000, 48,000 and 6800, respectively. tldD is a novel gene, but the tldE and zfiA genes proved to be the pmbA gene (production of Microcin B17) and the csrA gene (carbon storage regulator), respectively. (C) 1996 Academic Press Limited

3/7/37 (Item 9 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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04245399 Genuine Article#: RR111 Number of References: 28
Title: ANALYSIS OF EUKARYOTIC **TOPOISOMERASE-II** CLEAVAGE SITES IN THE
PRESENCE OF THE QUINOLONE CP-115,953 REVEALS DRUG-DEPENDENT AND

DRUG-INDEPENDENT RECOGNITION ELEMENTS

Author(s): SPITZNER JR; CHUNG IK; GOOTZ TD; MCGUIRK PR; MULLER MT
Corporate Source: OHIO STATE UNIV, DEPT MOLEC GENET, 484 W 12TH
AVE/COLUMBUS//OH/43210; OHIO STATE UNIV, DEPT MOLEC
GENET/COLUMBUS//OH/43210; PFIZER INC, DIV CENT RES, DEPT IMMUNOL & INFECT
DIS/GROTON//CT/06340
Journal: MOLECULAR PHARMACOLOGY, 1995, V48, N2 (AUG), P238-249
ISSN: 0026-895X
Language: ENGLISH Document Type: ARTICLE
Abstract: The quinolone derivative CP-115,953

[6,8-difluoro-7-(4-hydroxyphenyl)-1
-cyclopropyl-4-quinolone-3-carboxylic acid] has been shown to induce
eukaryotic **topoisomerase II**-mediated breaks in DNA, producing
cleavage patterns that are distinct from those induced by the
anticancer drugs amsacrine, etoposide, and teniposide. High levels of
the quinolone have been found to inhibit **topoisomerase II**
activity via an interaction with the enzyme and not by DNA unwinding.
Topoisomerase II cleavage sites were analyzed on nine DNA
fragments, and 85 quinolone-induced sites were sequenced, as well as 86
amsacrine and 134 teniposide sites. A consensus sequence was derived
for the quinolone sites that is different from those reported for other
drugs; however, because **topoisomerase II** cleavage sites are
double-stranded but not **palindromic**, different consensus
sequences are not easily compared. For this reason, a new,
double-stranded, consensus sequence method, the "unique-base
analysis," was developed; this was applied to the quinolone sites as
well as six other large sets of **topoisomerase II** sites determined
in the absence or presence of drugs. For each of the seven sets of
sites, conserved bases were found in the 16-base region spanning
positions -6 to +10, relative to the enzyme cleavage site (DNA breakage
between -1 and +1). The conserved bases were virtually identical in the
regions flanking the cleavage site for all seven data sets. In
contrast, the base preferences identified proximal to the cleavage
sites were unique to the drug tested. These observations suggest that
the selection of cleavage sites by **topoisomerase II** involves both
enzyme-dependent and drug-dependent recognition elements. The single
most preferred base in the quinolone sites was a cytosine at -1; the
same preference was found with teniposide, and 60 of the 85 quinolone
sites co-localized with teniposide sites.

3/7/38 (Item 10 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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04187922 Genuine Article#: RM104 Number of References: 42
Title: EFFECT OF ISOPROPYL-BETA-D-THIOGALACTOPYRANOSID INDUCTION OF THE LAC
OPERON ON THE SPECIFICITY OF SPONTANEOUS AND DOXORUBICIN-INDUCED
MUTATIONS IN ESCHERICHIA-COLI
Author(s): VEIGL ML; DONOVER SP; ANDERSON RD; AKST L; SEDWICK CE; SEDWICK
WD
Corporate Source: CASE WESTERN RESERVE UNIV, IRELAND CANC CTR, RES LABS, DEPT
MED, DIV HEMATOL ONCOL, UCRC BLDG 2/CLEVELAND//OH/44106; CASE WESTERN
RESERVE UNIV HOSP, IRELAND CANC CTR, DEPT MED/CLEVELAND//OH/44106; DEPT
VET AFFAIRS MED CTR/CLEVELAND//OH/00000
Journal: ENVIRONMENTAL AND MOLECULAR MUTAGENESIS, 1995, V26, N1, P16-25
ISSN: 0893-6692
Language: ENGLISH Document Type: ARTICLE

Abstract: Previous studies of doxorubicin-induced mutations employing F' lacI/lacO as an endogenous gene target have focused on properties of large deletions with 3' endpoints residing in the lacO region of the target gene. This study considers the influence of Lac repressor binding on the distribution of these deletions. Results of the DNA sequence level analysis of spontaneous and doxorubicin-induced i(-d) and lacO mutations in *Escherichia coli* uvrB(-) are reported for mutants isolated under conditions where Lac repression is relieved by isopropyl-beta-D-thiogalactopyranosid (IPTG; on inducer that prevents repressor binding to lacO). The location of deletions isolated from doxorubicin-treated cultures in the presence and absence of IPTG suggests that doxorubicin preferentially focuses deletion endpoints adjacent to its binding sites in lacO and that the distribution of these deletion endpoints is not modulated by Lac repressor binding. In contrast, spontaneous deletion endpoints are preferentially clustered in the loop away from the **palindromic** sequences under conditions of repression. However, when the Lac repressor/lacO binding complex is dissociated by IPTG, the spontaneous 3'-deletion endpoints distribute proportionally between the putative stem and loop of the lacO **palindrome**.

The single most striking effect of IPTG induction of the Lac operon was elimination of a 'hot spot' for T:A-->C:G transitions at position +6 in lacO. This base substitution 'hot spot,' which accounted for 17.6% of total doxorubicin-induced mutants and 16.4% of spontaneous mutants in repressed bacterial cultures, accounted for approximately 1% of total mutations in similar experiments carried out in the presence of IPTG. A large number of mutations at the +6 position are induced only by doxorubicin in the absence of IPTG, however, suggesting that both doxorubicin-induced and spontaneous mutation at this transition 'hot spot' are mediated by Lac repressor binding to lacO. (C) 1995 Wiley-Liss, Inc.

3/7/39 (Item 11 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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04006109 Genuine Article#: QY388 Number of References: 205
Title: BIME SEQUENCES - AN EXAMPLE OF ENTEROBACTERIAL REPETITIVE SEQUENCES
Author(s): BACHELLIER S
Corporate Source: INST PASTEUR, UNITE PROGRAMMAT MOLEC & TOXICOL
GENET, CNRS, URA 1444/F-75724 PARIS 15//FRANCE/
Journal: BULLETIN DE L INSTITUT PASTEUR, 1995, V93, N2 (APR-JUN), P97-152
ISSN: 0020-2452
Language: FRENCH Document Type: REVIEW

Abstract: Bacterial interspersed mosaic elements (or BIMEs) are repeated sequences identified in several enterobacterial genomes. BIMEs are a mosaic combination of small sequence motifs. It has been estimated that 500 BIMEs are scattered over the bacterial genome. BIMEs have been identified in several enterobacteria: *Escherichia coli*, *Salmonella typhimurium*, *Klebsiella* sp. and relatives of these bacteria. BIME function is not known, but their interactions with specific proteins (DNA polymerase I, **gyrase** and integration host factor) suggest that they could be involved in functional organization of bacterial chromosomes. Four other families of interspersed repetitive sequences have been shown to exist in a variety of bacterial genomes. Like BIMEs, these sequences are rather small, contain a region of dyad symmetry,

and are found in extragenic locations. Unlike BIMEs, IRU (or ERIC), box C sequences and RSA sequences occur in enterobacteria but also in other Gram-negative bacteria.

All these sequences are presented, potential functions of BIMEs are discussed, and possible relationships between the different elements are presented.

3/7/40 (Item 12 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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03802617 Genuine Article#: QG039 Number of References: 39
Title: CORRELATION OF DOXORUBICIN FOOTPRINTS WITH DELETION END-POINTS IN
LAC0 OF ESCHERICHIA-COLI
Author(s): SEDWICK WD; ANDERSON RD; BAXTER J; DONOVER S; SCHNEITER S; VEIGL
ML
Corporate Source: CASE WESTERN RESERVE UNIV,CASE WESTERN RESERVE VET
HOSP,DEPT MED,UCRC BLDG 2,SUITE 200/CLEVELAND//OH/44106; UNIV CLEVELAND
HOSP,Ireland CANC CTR/CLEVELAND//OH/00000
Journal: MUTATION RESEARCH-FUNDAMENTAL AND MOLECULAR MECHANISMS OF
MUTAGENESIS, 1995, V326, N1 (JAN), P17-27
ISSN: 0027-5107
Language: ENGLISH Document Type: ARTICLE

Abstract: This study explored the possibility that the sequence location of doxorubicin-induced deletion endpoints might relate to DNA structural alterations caused by doxorubicin binding to DNA. The 3'-OH endpoints of doxorubicin-induced deletions terminating in the 35-bp region of lacO appear to distribute differently from spontaneous deletion endpoints. Doxorubicin-induced deletions focus in the 26-bp **palindrome** which is separated by a 9-bp region with no reverse complementary, whereas spontaneous deletion 3'-OH endpoints are found distributed throughout the operator region. In order to explore the mechanism of deletion induction by doxorubicin, drug footprinting studies were carried out with DNA labeled at the 5' end of each of the complementary DNA strands encompassed by lacO. Doxorubicin protected the 9-bp region between the **palindromic** sequences from DNase I cutting and caused enhanced DNase I cleavage at symmetrical sites in the **palindrome**, which were inherently resistant to the nuclease in the absence of the drug. These symmetrical sites also define regions in which the occurrence of deletion endpoints is enhanced 6-fold in the presence of doxorubicin. This enhanced cutting and mutation occur in regions of the **palindrome** that are flanked by expected doxorubicin binding sites, but are not themselves binding sites of the drug. Similarly, other sites where the frequency of deletion endpoints increased in response to doxorubicin occurred directly adjacent to regions where doxorubicin appeared to inhibit cutting by DNase I. These results suggest that the binding of doxorubicin in the **palindrome** directs both the frequency and the specificity of deletion formation in this gene region.

3/7/41 (Item 13 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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03534278 Genuine Article#: PK931 Number of References: 67

Title: ESCHERICHIA-COLI TYRT GENE-TRANSCRIPTION IS SENSITIVE TO DNA
SUPERCOILING IN ITS NATIVE CHROMOSOMAL CONTEXT - EFFECT OF DNA
TOPOISOMERASE-IV OVEREXPRESSION ON TYRT PROMOTER FUNCTION

Author(s): FREE A; DORMAN CJ

Corporate Source: UNIV DUBLIN TRINITY COLL, MOYNE INST PREVENT MED, DEPT
MICROBIOL/DUBLIN 2//IRELAND/; UNIV DUBLIN TRINITY COLL, MOYNE INST
PREVENT MED, DEPT MICROBIOL/DUBLIN 2//IRELAND/

Journal: MOLECULAR MICROBIOLOGY, 1994, V14, N1 (OCT), P151-161

ISSN: 0950-382X

Language: ENGLISH Document Type: ARTICLE

Abstract: We have investigated the in vivo DNA supercoiling sensitivity of the Escherichia coli trnA(1) (tyr) gene (tyrT) promoter in its normal chromosomal location. Here, the native tyrT promoter is found to be exquisitely sensitive to mutations and to drugs which alter the level of DNA supercoiling. We show that the response of the tyrT promoter to supercoiling is qualitatively similar to that of a known supercoiling-sensitive trnA gene promoter, hisR. Specifically, treatments which increase in vivo DNA supercoiling levels enhance transcription of these trnA genes. Particularly striking is the strong enhancement of expression from both promoters by a transposon insertion mutation in the topA gene encoding DNA **topoisomerase** I. This phenotypic effect can be complemented by providing active **topoisomerase** I in trans from a recombinant plasmid. Interestingly, it can also be complemented by overexpression of the genes encoding the subunits of DNA **topoisomerase** IV. We believe that this is the first demonstration that DNA **topoisomerase** IV can influence gene expression and it suggests that DNA **topoisomerase** I is partially redundant, at least in E. coli.

3/7/42 (Item 14 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci

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02811861 Genuine Article#: MF289 Number of References: 40

Title: THEORETICAL DESIGN OF A BIS-ORTHOPEPTIDE DERIVATIVE OF A
TETRACATIONIC PORPHYRIN TARGETED TOWARD A 6-BASE PAIR SEQUENCE OF DNA

Author(s): HUI XW; GRESH N

Corporate Source: INST BIOL PHYSICOCHEM, BIOCHIM THEOR LAB, 13 RUE PIERRE &
MARIE CURIE/F-75005 PARIS//FRANCE/

Journal: JOURNAL OF BIOMOLECULAR STRUCTURE & DYNAMICS, 1993, V11, N2 (OCT)
, P333-344

ISSN: 0739-1102

Language: ENGLISH Document Type: ARTICLE

Abstract: Tetra-(4-N-methylpyridyl)-porphyrin, (T4MPyP), is a tetracationic porphyrin that binds to G-C sequences of DNA by means of an intercalative mode. In order to extend its selective sequence recognition capacity for bases beyond the intercalation site, and in the major groove, we have undertaken the theoretical design of bis-ortho peptide derivatives of T4MPyP. In these, two ortho N-methylpiperidinium nitrogens are linked to a cationic residue, L-Lys, L-Orn, or L-Arg. The binding energetics of these novel compounds were compared for six distinct double-stranded **palindromic** hexanucleotide sequences. Four distinct modes of binding were compared: a) major, b) minor groove binding of both peptidic arms; c) a straddling mode in which each arm is in a different groove of DNA; d) exclusive binding of the arms to the sugar-phosphate backbone. For our most promising compound, that with Lys sidechains, a distinctive

energetical advantage was computed in favor of an all-major groove binding to sequence d(CCCGGG)2. The corresponding complex is separated by an energy gap of 12 kcal/mol, with respect to the second-best sequence bound in the major groove, d(GGCGCC)2, and of 20 kcal/mol with respect to minor groove binding to sequence d(TACGTA)2. The results obtained with such a prototypic compound indicate that it is fully possible to design sequence selective (> 6 base-pairs) photosensitizers as peptide derivatives of T4MPyP and prompt the engineering of further, more complex analogs thereof.

3/7/43 (Item 15 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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02777246 Genuine Article#: MC809 Number of References: 41
Title: AUTOREGULATION-DEFICIENT MUTANT OF THE PLASMID R6K-ENCODED PI-PROTEIN DISTINGUISHES BETWEEN **PALINDROMIC** AND NONPALINDROMIC BINDING-SITES
Author(s): YORK D; FILUTOWICZ M
Corporate Source: UNIV WISCONSIN, DEPT BACTERIOL, EB FRED HALL, 1550 LINDEN DR/MADISON//WI/53706; UNIV WISCONSIN, DEPT BACTERIOL, EB FRED HALL, 1550 LINDEN DR/MADISON//WI/53706
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1993, V268, N29 (OCT 15), P 21854-21861
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE
Abstract: The autogenously regulated gene *pir* of *Escherichia coli* plasmid R6K encodes the replication protein *pi*. This protein binds to two sites in the operator region of the *pir* gene: a 22-base pair nonpalindromic sequence and a pair of **palindromic** 9-base pair sequences. These *pi*-binding sites are similar, suggesting that *pi* uses a single DNA-binding domain in recognizing them. We devised a plasmid system permitting isolation of mutants of the *pi* protein which are altered in autoregulation. A Ser87 to Asn substitution in one such mutant, designated *pi*87, reduces the protein's ability to repress the *pir* gene promoter in vivo. DNase I protection and gel retardation assays were carried out with highly purified *pi*87 protein. In these studies *pi*87 exhibited altered binding to the **palindromic** but not to the nonpalindromic part of the operator of the *pir* gene. Chemical cross-linking and gel filtration analyses have shown that the dimerization properties of wild type *pi* and *pi*87 proteins are similar in solution. We propose that the interaction of *pi* protein with the **palindromic** part of the *pir* operator is essential for autoregulation; we also propose that there is a fundamental difference in the mechanisms of *pi* protein recognition of **palindromic** and nonpalindromic sequences.

3/7/44 (Item 16 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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02767922 Genuine Article#: MB916 Number of References: 49
Title: INTEGRATION HOST FACTOR BINDS TO A UNIQUE CLASS OF COMPLEX REPETITIVE EXTRAGENIC DNA-SEQUENCES IN *ESCHERICHIA-COLI*
Author(s): OPPENHEIM AB; RUDD KE; MENDELSON I; TEFF D
Corporate Source: HEBREW UNIV JERUSALEM, HADASSAH MED SCH, DEPT MOLEC

GENET/IL-91010 JERUSALEM//ISRAEL//; NATL LIB MED,NATL CTR BIOTECHNOL
INFORMAT/BETHESDA//MD/20894

Journal: MOLECULAR MICROBIOLOGY, 1993, V10, N1 (OCT), P113-122

ISSN: 0950-382X

Language: ENGLISH Document Type: ARTICLE

Abstract: Interspersed repeated DNA sequences are characteristic features of both prokaryotic and eukaryotic genomes. REP sequences are defined as conserved repetitive extragenic **palindromic** sequences and are found in *Escherichia coli*, *Salmonella typhimurium* and other closely related enteric bacteria. These REP sequences may participate in the folding of the bacterial chromosome. In this work we describe a unique class of 28 conserved complex REP clusters, about 100 bp long, in which two inverted REPs are separated by a singular integration host factor (IHF) recognition sequence. We term these sequences RIP (for repetitive IHF-binding **palindromic**) elements and demonstrate that IHF binds to them specifically. It is estimated that there are about 70 RIP elements in *E. coli*. Our analysis shows that the RIP elements are evenly distributed around the bacterial chromosome. The possible function of the RIP element is discussed.

3/7/45 (Item 17 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci

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02745975 Genuine Article#: MA818 Number of References: 26

Title: EXCISION-REPAIR REDUCES DOXORUBICIN-INDUCED GENOTOXICITY

Author(s): ANDERSON RD; VEIGL ML; BAXTER J; SEDWICK WD

Corporate Source: CASE WESTERN RESERVE UNIV, IRELAND CANC CTR RES LABS, UCRC
BLDG 2, SUITE 200, 11001 CEDAR RD/CLEVELAND//OH/44106; CASE WESTERN
RESERVE UNIV, IRELAND CANC CTR RES LABS, UCRC BLDG 2, SUITE 200, 11001
CEDAR RD/CLEVELAND//OH/44106

Journal: MUTATION RESEARCH, 1993, V294, N3 (OCT), P215-222

ISSN: 0921-8262

Language: ENGLISH Document Type: ARTICLE

Abstract: LacI mutations induced by doxorubicin in a wild-type, *uvr(A)BC* repair-proficient *E. coli* strain were analyzed by DNA sequencing. These mutations were contrasted with mutations previously recovered from doxorubicin-treated *uvrB*- organisms in order to assess the role of excision repair in doxorubicin-induced genotoxicity. After a 30-min exposure of wild-type *E. coli* to 330 μ M doxorubicin, survival was 34% and the overall lacI mutation frequency increased 1.8-fold to 340×10^{-8} . The distribution of doxorubicin-induced mutants among subclasses of mutation involving the *i*(-d) and lac operator regions differed significantly between repair-proficient and -deficient strains. Distributional differences appeared to result both from a decrease in deletions involving the lac operator and an increase in base substitutions involving the *i*(-d) region in repair proficient organisms. However, elements of the doxorubicin-induced mutation spectrum in *uvrB*- *E. coli* are still discernable in wild-type organisms. These elements include the remarkable shift of 3'-deletion endpoints to **palindromic** sequence within the lac operator and the recovery of multiple isolates of T:A --> A:T transversions at position 96 in doxorubicin-treated cultures. These observations suggest that components of the *uvr(A)BC* nucleotide excision repair system function through a general mechanism prior to fixation of mutations to reduce, but not completely eliminate, the genotoxic effects of doxorubicin.

3/7/46 (Item 18 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02696424 Genuine Article#: LX116 Number of References: 51
Title: MINIMAL ESSENTIAL ORIGIN OF PLASMID pSC101 REPLICATION - REQUIREMENT
OF A REGION DOWNSTREAM OF ITERONS
Author(s): SUGIURA S; OHKUBO S; YAMAGUCHI K
Corporate Source: KANAZAWA UNIV, INST GENE RES/KANAZAWA/ISHIKAWA 920/JAPAN/;
KANAZAWA UNIV, INST GENE RES/KANAZAWA/ISHIKAWA 920/JAPAN/
Journal: JOURNAL OF BACTERIOLOGY, 1993, V175, N18 (SEP), P5993-6001
ISSN: 0021-9193
Language: ENGLISH Document Type: ARTICLE

Abstract: The minimal replication origin (ori) of the plasmid pSC101 was defined as an about 220-bp region under the condition that the Rep (or RepA) protein, a plasmid-encoded initiator protein, was supplied in trans. The DnaA box is located at one end of ori, as in other plasmids, like mini-F and Pl. The other border is a strong binding site (IR-1) of Rep which is a **palindromic** sequence and lies in an about 50-bp region beyond the repeated sequences (iterons) in ori. This IR-1 is located just upstream of another strong Rep binding site (IR-2), the operator site of the structure gene of Rep (rep), but its function has not been determined. The present study shows that the IR-1 sequence capable of binding to Rep is essential for plasmid replication with a nearly normal copy number. Furthermore, a region between the third iteron and IR-1 is also required in a sequence-specific fashion, since some one-base substitutions in this region inactivate the origin function. It is likely that the region also is a recognition site of an unknown protein. Three copy number mutations of rep can suppress any one-base substitution mutation. On the other hand, the sequence of a spacer region between the second and the third iterons, which is similar to that of the downstream region of the third iteron, can be changed without loss of the origin function. The requirement of the region downstream of iterons in pSC101 seems to be unique among iteron-driven plasmid replicons.

3/7/47 (Item 19 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02320244 Genuine Article#: KT913 Number of References: 81
Title: INTERSPERSION OF AN UNUSUAL GCN4 ACTIVATION SITE WITH A COMPLEX
TRANSCRIPTIONAL REPRESSION SITE IN TY2 ELEMENTS OF
SACCHAROMYCES-CEREVISIAE
Author(s): TURKEL S; FARABAUGH PJ
Corporate Source: UNIV MARYLAND, DEPT BIOL SCI/CATONSVILLE//MD/21228; UNIV
MARYLAND, DEPT BIOL SCI/CATONSVILLE//MD/21228
Journal: MOLECULAR AND CELLULAR BIOLOGY, 1993, V13, N4 (APR), P2091-2103
ISSN: 0270-7306
Language: ENGLISH Document Type: ARTICLE

Abstract: Transcription of the Ty2-917 retrotransposon of *Saccharomyces cerevisiae* is modulated by a complex set of positive and negative elements, including a negative region located within the first open reading frame, TYA2. The negative region includes three downstream repression sites (DRSI, DRSII, and DRSIII). In addition, the negative region includes at least two downstream activation sites (DASs). This

paper concerns the characterization of DASI. A 36-bp DASI oligonucleotide acts as an autonomous transcriptional activation site and includes two sequence elements which are both required for activation. We show that these sites bind in vitro the transcriptional activation protein GCN4 and that their activity in vivo responds to the level of GCN4 in the cell. We have termed the two sites GCN4 binding sites (GBS1 and GBS2). GBS1 is a high-affinity GCN4 binding site (dissociation constant, approximately 25 nM at 30-degrees-C), binding GCN4 with about the affinity of a consensus UAS(GCN4), this though GBS1 includes two differences from the right half of the **palindromic** consensus site. GBS2 is more diverged from the consensus and binds GCN4 with about 20-fold-lower affinity. Nucleotides 13 to 36 of DASI overlap DRSII. Since DRSII is a transcriptional repression site, we tested whether DASI includes repression elements. We identify two sites flanking GBS2, both of which repress transcription activated by the consensus GCN4-specific upstream activation site (UAS(GCN4)). One of these is repeated in the 12 bp immediately adjacent to DASI. Thus, in a 48-bp region of Ty2-917 are interspersed two positive and three negative transcriptional regulators. The net effect of the region must depend on the interaction of the proteins bound at these sites, which may include their competing for binding sites, and on the physiological control of the activity of these proteins.

3/7/48 (Item 20 from file: 34)
 DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02228578 Genuine Article#: KM161 Number of References: 14
 Title: LYMPHOID-V(D)J RECOMBINATION - FUNCTIONAL-ANALYSIS OF THE SPACER
 SEQUENCE WITHIN THE RECOMBINATION SIGNAL

Author(s): WEI Z; LIEBER MR

Corporate Source: STANFORD UNIV,MED CTR,SCH MED,DEPT PATHOL,EXPTLONCOL
 LAB/STANFORD//CA/94305; STANFORD UNIV,MED CTR,SCH MED,DEPT
 PATHOL,EXPTLONCOL LAB/STANFORD//CA/94305

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1993, V268, N5 (FEB 15), P
 3180-3183

ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE

Abstract: The V(D)J recombination reaction is directed by a pair of signal sequences, each consisting of a **palindromic** heptamer, an A/T-rich nonamer, and an intervening spacer sequence of 12 or 23 base pairs. The spacer sequence previously has not been analyzed for a functional role. In this study, numerous simultaneous sequence changes have been made in the spacer of each signal to test their functional importance. All of the AT base pairs in each signal were changed to GC base pairs. This particular change is of interest because it markedly increases the energy that would be required to melt out the two strands of each signal to permit the intersignal base pairing proposed in a commonly invoked model for signal-signal interaction in V(D)J recombination. We find that changing 6 of 12 AT base pairs in the 12-signal to GC does not affect V(D)J recombination, nor does changing 11 of 23 AT base pairs in the 23-signal. Substrates with all-GC spacer sequences in both the 12- and the 23-signal also recombine at efficiencies that are not significantly reduced. These studies demonstrate that the sequences at these particular positions are not recognized by the recombinase. In addition, the data do not support models invoking signal-signal base pairing.

3/7/49 (Item 21 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

02226359 Genuine Article#: KM162 Number of References: 53
Title: HIGH-AFFINITY DNA-BINDING MYC ANALOGS - RECOGNITION BY AN
ALPHA-HELIX

Author(s): FISHER DE; PARENT LA; SHARP PA
Corporate Source: MIT,CTR CANC RES,DEPT BIOL/CAMBRIDGE//MA/02139; CHILDRENS
HOSP MED CTR,DEPT PEDIAT HEMATOL & ONCOL/BOSTON//MA/02115; HARVARD
UNIV,SCH MED,DANA FARBER CANC INST,DEPTPEDIAT HEMATOL &
ONCOL/BOSTON//MA/02115

Journal: CELL, 1993, V72, N3 (FEB 12), P467-476

ISSN: 0092-8674

Language: ENGLISH Document Type: ARTICLE

Abstract: Myc and other basic-helix-loop-helix-leucine zipper (b-HLH-ZIP) proteins bind the sequence CACGTG. Exhaustive mutagenesis in the basic domain identified four amino acids critical for DNA binding with spacing suggestive of an alpha-helical face. Surprisingly, two highly conserved amino acids were nonessential for DNA binding. Circular dichroism demonstrated a DNA-induced alpha-helical transition. A series of analogs were constructed with multiple simultaneous alanine substitutions at nonessential positions and a critical lysine for arginine substitution. In this way 35-fold higher specific affinity for CACGTG was obtained as compared with the basic domain of c-Myc. These b-HLH-ZIP proteins appear to bind the same **palindromic** sequence and may compete for common sites in vivo. Additionally, a C-terminal basic region clamp motif was identified that was also identifiable in crystal structures from several different families of DNA-binding factors.

3/7/50 (Item 22 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

02215768 Genuine Article#: KK976 Number of References: 46
Title: PROTEIN HU BINDS SPECIFICALLY TO KINKED DNA

Author(s): PONTIGGIA A; NEGRI A; BELTRAME M; BIANCHI ME
Corporate Source: UNIV MILAN,DIPARTIMENTO GENET & BIOL MICRORGAN,VIA
CELORIA 26/I-20133 MILAN//ITALY//; UNIV MILAN,DIPARTIMENTO GENET & BIOL
MICRORGAN,VIA CELORIA 26/I-20133 MILAN//ITALY//; OSPED SAN RAFFAELE,IST
SCI/I-20132 MILAN//ITALY//; UNIV MILAN,IST FISIOL V & BIOCHIM/I-20133
MILAN//ITALY//

Journal: MOLECULAR MICROBIOLOGY, 1993, V7, N3 (FEB), P343-350

ISSN: 0950-382X

Language: ENGLISH Document Type: ARTICLE

Abstract: We have purified the main four-way junction DNA-binding protein of Escherichia coli, and have found it to be the well-known HU protein. HU protein recognizes with high-affinity one of the angles present in the junction, a molecule with the shape of an X. Other DNA structures characterized by sharp bends or kinks, like bulged duplex DNAs containing unpaired bases, are also bound. HU protein appears to inhibit cruciform extrusion from supercoiled inverted repeat (**palindromic**) DNA, either by constraining supercoiling or by trapping a metastable interconversion intermediate. All these

properties are analogous to the properties of the mammalian chromatin protein HMG1. We suggest that HU is a prokaryotic HMG1-like protein rather than a histone-like protein.

3/7/51 (Item 23 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02127316 Genuine Article#: KD073 Number of References: 45
Title: PURIFICATION AND CHARACTERIZATION OF DNA **TOPOISOMERASE**-IV IN
ESCHERICHIA-COLI
Author(s): KATO J; SUZUKI H; IKEDA H
Corporate Source: UNIV TOKYO, INST MED SCI, DEPT MOLEC BIOL, PO TAKANAWA/TOKYO
108//JAPAN/; KANAGAWA UNIV, DEPT APPL
BIOL/HIRATSUKA/KANAGAWA25912/JAPAN/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N36 (DEC 25), P
25676-25684
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE
Abstract: The subunits of **topoisomerase** IV (topo IV), the ParC and
ParE proteins in Escherichia coli, were purified to near homogeneity
from the respective overproducers. They revealed type II
topoisomerase activity only when they were combined with each
other. In the presence of Mg2+ and ATP, topo IV was capable of relaxing
a negatively or positively supercoiled plasmid DNA or converting the
knotted P4 phage DNA, whether nicked or ligated, to a simple ring.
However, supercoiling activity was not detected. The
topoisomerase activity was not detectable when the purified ParC
and ParE proteins were combined with the purified GyrB and GyrA
proteins, respectively. This is consistent with the result that neither
a parC nor a parE mutation was compensated by transformation with a
plasmid carrying either the gyrA or the gyrB gene. Simultaneous
introduction of both the gyrA and gyrB plasmids corrected the
phenotypic defect of parC and parE mutants. The results suggest that
DNA **gyrase** can substitute for topo IV at least in some part of
the function for chromosome partitioning. Antisera were prepared
against the purified ParC, ParE, GyrA, and GyrB proteins and used to
investigate cellular localization of these gene products. ParC protein
was found to be specifically associated with inner membranes only in
the presence of DNA. This result suggests that one of the functions of
topo IV might be to anchor chromosomes on membranes as previously
proposed for eukaryotic **topoisomerase** II.

3/7/52 (Item 24 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02046306 Genuine Article#: JW772 Number of References: 39
Title: DNA-BASE SEQUENCE CHANGES IN SPONTANEOUS AND ETHYL
METHANESULFONATE-INDUCED MUTATIONS OF A CHROMOSOMALLY-INTEGRATED GENE
IN CHINESE-HAMSTER OVARY CELLS
Author(s): ASHMAN CR
Corporate Source: UNIV CHICAGO, DEPT RADIAT & CELLULAR ONCOL, 5841 S MARYLAND
AVE, POB 442/CHICAGO//IL/60637
Journal: MUTATION RESEARCH, 1992, V270, N2 (NOV 16), P115-124
ISSN: 0921-8262

Language: ENGLISH Document Type: ARTICLE

Abstract: A series of spontaneous and ethyl methanesulfonate-induced 6-thioguanine-resistant mutants were isolated in the CHO-10T5 cell line. This cell line was constructed by the introduction of a shuttle vector containing the Escherichia coli gpt gene into a hypoxanthine-guanine phosphoribosyltransferase deficient derivative of the Chinese hamster cell line CHO-K1. Shuttle vector sequences were recovered from many of the mutant cell lines by the COS cell fusion technique and the DNA base sequence of the gpt genes was determined whenever possible.

The base sequences were determined for gpt genes recovered from 29 spontaneous mutants. Of these 29 mutants, 9 have single base substitutions, 1 has a small duplication, 17 have simple deletions, 1 has a deletion with additional bases inserted at the deletion site, and 1 has no change in the gpt coding sequence. Many of the deletions were less than 20 basepairs in length and several occurred in a region previously observed to be a hotspot for spontaneous deletions. The generation of the deletion/insertion mutation may have involved a quasi-palindromic intermediate.

A total of 59 ethyl methanesulfonate-induced mutants were isolated and vector sequences were recovered from 50 mutants. All 50 mutants sequenced has single base substitutions and most (45) were G:C to A:T transitions. While there were no strong hotspots in this collection of mutations, the site distribution was obviously nonrandom. Many of the G:C to A:T transitions either produced a nonsense codon or occurred at glycine codons.

3/7/53 (Item 25 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01906822 Genuine Article#: JL053 Number of References: 31
Title: OVEREXPRESSION AND RAPID PURIFICATION OF THE ORFE/RPH GENE-PRODUCT,
RNASE PH OF ESCHERICHIA-COLI
Author(s): JENSEN KF; ANDERSEN JT; POULSEN P
Corporate Source: UNIV COPENHAGEN, INST BIOL CHEM, DIV ENZYME, SOLVGADEN
83/DK-1307 COPENHAGEN K//DENMARK/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N24 (AUG 25), P
17147-17152
ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE

Abstract: The pyrE gene, encoding the pyrimidine biosynthetic enzyme orotate phosphoribosyltransferase, is the promoter distal gene of the dicistronic orfE-pyrE operon. The promoter proximal orfE gene, whose transcription and translation is important for regulation of the pyrE attenuator, encodes a 238-amino acid residue protein which was recently identified as the phosphorolytic ribonuclease, RNase PH, that removes nucleotides from the 3' ends of tRNA precursors. In this paper we report the construction of a plasmid, which overexpresses the orfE and pyrE gene products substantially, as well as the purification of the OrfE protein by ammonium sulfate precipitation and chromatography on phosphocellulose. The highly purified protein catalyzes the phosphorolytic cleavage of poly(A) at a rate of 1.6- μ mol/min/mg and the formation of CDP from tRNA-CCA-C(n) and orthophosphate at a rate equal to 0.14- μ mol/min/mg, as characteristic for RNase PH. OrfE/RNase

PH contains helix-turn-helix motifs resembling those in DNA-binding proteins, and it binds nonspecifically to DNA. On SDS gels, Orfe/RNase PH migrates as two distinct protein bands. This heterogeneity might be caused by post-translational modification other than proteolysis, or may be an electrophoretic artifact. The native protein is composed of two or more subunits.

3/7/54 (Item 26 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01834847 Genuine Article#: JE399 Number of References: 44
Title: PHYSICAL MAPPING OF REPETITIVE EXTRAGENIC **PALINDROMIC** SEQUENCES IN ESCHERICHIA-COLI AND PHYLOGENETIC DISTRIBUTION AMONG ESCHERICHIA-COLI STRAINS AND OTHER ENTERIC BACTERIA
Author(s): DIMRI GP; RUDD KE; MORGAN MK; BAYAT H; AMES GFL
Corporate Source: UNIV CALIF BERKELEY, DEPT MOLEC & CELL BIOL, DIV BIOCHEM & MOLEC BIOL, 401 BARKER HALL/BERKELEY//CA/94720; UNIV CALIF BERKELEY, DEPT MOLEC & CELL BIOL, DIV BIOCHEM & MOLEC BIOL, 401 BARKER HALL/BERKELEY//CA/94720; NATL LIB MED, NATL CTR BIOTECHNOL INFORMAT/BETHESDA//MD/20894

Journal: JOURNAL OF BACTERIOLOGY, 1992, V174, N14 (JUL), P4583-4593

Language: ENGLISH Document Type: ARTICLE

Abstract: Repetitive extragenic **palindromic** (REP) sequences are highly conserved inverted repeat sequences originally discovered in Escherichia coli and Salmonella typhimurium. We have physically mapped these sequences in the E. coli genome by using Southern hybridization of an ordered phage bank of E. coli (Y. Kohara, K. Akiyama, and K. Isono, Cell 50:495-508, 1987) with generic REP probes derived from the REP consensus sequence. The set of REP probe-hybridizing clones was correlated with a set of clones expected to contain REP sequences on the basis of computer searches. We also show that a generic REP probe can be used in Southern hybridization to analyze genomic DNA digested with restriction enzymes to determine genetic relatedness among natural isolates of E. coli. A search for these sequences in other members of the family Enterobacteriaceae shows a consistent correlation between both the number of occurrences and the hybridization strength and genealogical relationship.

3/7/55 (Item 27 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01725254 Genuine Article#: HV726 Number of References: 86
Title: HELIX OPENING TRANSITIONS IN SUPERCOILED DNA
Author(s): MURCHIE AIH; BOWATER R; ABOULELA F; LILLEY DMJ
Corporate Source: UNIV DUNDEE, DEPT BIOCHEM/DUNDEE DD1 4HN//SCOTLAND/; UNIV DUNDEE, DEPT BIOCHEM/DUNDEE DD1 4HN//SCOTLAND/
Journal: BIOCHIMICA ET BIOPHYSICA ACTA, 1992, V1131, N1 (MAY 7), P1-15
Language: ENGLISH Document Type: REVIEW

3/7/56 (Item 28 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01608178 Genuine Article#: HL490 Number of References: 47

Title: TANDEM REPEATS IN EXTRACHROMOSOMAL RIBOSOMAL DNA OF
DICTYOSTELIUM-DISCOIDEUM, RESULTING FROM CHROMOSOMAL MUTATIONS

Author(s): COLE RA; WILLIAMS KL

Corporate Source: MACQUARIE UNIV, SCH BIOL SCI/SYDNEY/NSW 2109/AUSTRALIA/

Journal: GENETICS, 1992, V130, N4 (APR), P757-769

Language: ENGLISH Document Type: ARTICLE

Abstract: Extrachromosomal ribosomal DNA in the simple eukaryote

Dictyostelium discoideum is readily separated from chromosomal DNA by orthogonal field electrophoresis (OFAGE), forming a prominent band in the 110-kb region of the gel. Here we show that mutations in at least two chromosomal genes give rise to a ladder of rDNA bands increasing in size up to about 300 kb. One of these mutations, the rrcA350 allele, which is recessive to wild type and maps to the centromere-proximal region of linkage group II, has an unstable phenotype; spontaneous revertants, which no longer exhibit the rDNA ladder, have been recovered. Another mutation rrc-351, provisionally mapped to linkage group IV, is dominant to wild type. The rDNA ladder is caused by concatamerization of a 34-kb fragment in the nontranscribed central spacer region of the 88-kb linear rDNA **palindrome**. Restriction enzyme analysis has revealed that each concatamer is generated by crossovers between two rDNA molecules.

3/7/57 (Item 29 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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01510054 Genuine Article#: HE459 Number of References: 40

Title: PROPAGATION OF PSC101 PLASMIDS DEFECTIVE IN BINDING OF INTEGRATION
HOST FACTOR

Author(s): BIEK DP; COHEN SN

Corporate Source: UNIV KENTUCKY, MED CTR, DEPT MICROBIOL &
IMMUNOL/LEXINGTON//KY/40536; STANFORD UNIV, MED CTR, SCH MED, DEPT
GENET/STANFORD//CA/94305

Journal: JOURNAL OF BACTERIOLOGY, 1992, V174, N3 (FEB), P785-792

Language: ENGLISH Document Type: ARTICLE

Abstract: Integration host factor (IHF), a multifunctional protein of *E. coli*, normally is required for the replication of plasmid pSC101. T. T. Stenzel, P. Patel, and D. Bastia (Cell 49:709-717, 1987) have reported that IHF binds to a DNA locus near the pSC101 replication origin and enhances a static bend present in this region; mutation of the IHF binding site affects the plasmid's ability to replicate. We report here studies indicating that the requirement for IHF binding near the pSC101 replication origin is circumvented partially or completely by (i) mutation of the plasmid-encoded repA (replicase) gene or the chromosomally encoded topA gene, (ii) the presence on the plasmid of the pSC101 partition (par) locus, or (iii) replacement of the par locus by a strong transcriptional promoter. With the exception of the repA mutation, the factors that substitute for a functional origin region IHF binding site are known to alter plasmid topology by increasing negative DNA supercoiling, as does IHF itself. These results are consistent with the proposal that IHF binding near the pSC101 replication origin promotes plasmid replication by inducing a conformational change leading to formation of a repA-dependent DNA-protein complex. A variety of IHF-independent mechanisms can facilitate formation of the putative replication-initiation complex.

3/7/58 (Item 30 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01348813 Genuine Article#: GR723 Number of References: 61
Title: ON THE DELETION OF INVERTED REPEATED DNA IN ESCHERICHIA-COLI -
EFFECTS OF LENGTH, THERMAL-STABILITY, AND CRUCIFORM FORMATION INVIVO
Author(s): SINDEN RR; ZHENG GX; BRANKAMP RG; ALLEN KN
Corporate Source: UNIV CINCINNATI, COLL MED, DEPT MOLEC GENET BIOCHEM &
MICROBIOL/CINCINNATI//OH/45267
Journal: GENETICS, 1991, V129, N4, P991-1005
Language: ENGLISH Document Type: ARTICLE
Abstract: We have studied the deletion of inverted repeats cloned into the
Eco RI site within the CAT gene of plasmid pBR325. A cloned inverted
repeat constitutes a **palindrome** that includes both Eco RI sites
flanking the insert. In addition, the two Eco RI sites represent
direct repeats flanking a region of **palindromic** symmetry. A
current model for deletion between direct repeats involves the
formation of DNA secondary structure which may stabilize the
misalignment between the direct repeats during DNA replication. Our
results are consistent with this model. We have analyzed deletion
frequencies for several series of inverted repeats, ranging from 42 to
106 bp, that were designed to form cruciforms at low temperatures and
at low superhelical densities. We demonstrate that length, thermal
stability of base pairing in the hairpin stem, and ease of cruciform
formation affect the frequency of deletion. In general, longer
palindromes are less stable than shorter ones. The deletion
frequency may be dependent on the thermal stability of base pairing
involving approximately 16-20 bp from the base of the hairpin stem.
The formation of cruciforms in vivo leads to a significant increase in
the deletion frequency. A kinetic model is presented to describe the
relationship between the physical-chemical properties of DNA structure
and the deletion of inverted repeats in living cells.

3/7/59 (Item 31 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01123096 Genuine Article#: FY287 Number of References: 57
Title: DNA-SEQUENCE SPECIFICITY OF DOXORUBICIN-INDUCED MUTATIONAL DAMAGE IN
UVRB- ESCHERICHIA-COLI
Author(s): ANDERSON RD; VEIGL ML; BAXTER J; SEDWICK WD
Corporate Source: UNIV HOSP CLEVELAND, IRELAND CANC CTR, RES LABS, UNIV CIRCLE
RES CTR, BLDG 2/CLEVELAND//OH/44106; UNIV HOSP CLEVELAND, IRELAND CANC
CTR, RES LABS, UNIV CIRCLE RES CTR, BLDG 2/CLEVELAND//OH/44106; CASE
WESTERN RESERVE UNIV, DEPT MED/CLEVELAND//OH/44106
Journal: CANCER RESEARCH, 1991, V51, N15, P3930-3937
Language: ENGLISH Document Type: ARTICLE
Abstract: In the absence of excision repair, doxorubicin caused a striking
(41-fold) increase in the frequency of large deletion mutations
extending from the lac operator (lacO) into the lac repressor gene
(lacI) of Escherichia coli. In contrast, there was only a 2-fold
increase in the frequency of small deletions despite a 3-fold increase
in overall mutation frequency. The 5'-endpoints of doxorubicin-induced
lacO and lacI/lacO deletions occurred at the DNA sequence 5'-pyTAA or
5'-AATpy (where py is pyrimidine) (16%), at runs of purines or

pyrimidines (41%) and adjacent to 5'-dGdC or 5'-dCdG doublets (34%). Ninety % (27 of 30) of the doxorubicin-induced deletions involving the region of the lacO **palindrome** had 3'-endpoints within the **palindrome** sequence as compared with 40% (4 of 10) spontaneous deletions in an untreated set. Doxorubicin-induced single base substitutions were highly focused at one site (4 of 6) in the i(-d) region of lacI, in contrast to the spontaneous distribution of point mutations, where 16 mutants were recovered at 12 different sites. An increased frequency (3-fold) of highly focused base substitutions was also observed at 2 sites in the lac operator region (at lacO +6, which is a transition "hotspot" in the spontaneous spectra of both wild type and uvrB- organisms and at the adjacent +5 site). Notably, the frequency of 1- and 2-base frameshifts did not increase in the doxorubicin-induced spectrum, relative to the spontaneous mutation spectrum. These in vivo observations in E. coli suggest that in the absence of excision repair, doxorubicin causes highly focused deletions and base substitutions. These mutations occur adjacent to DNA sequences identified in previous in vitro studies as preferential sites of doxorubicin binding.

3/7/60 (Item 32 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01057381 Genuine Article#: FR949 Number of References: 57
Title: DNA CRUCIFORMS AND THE NUCLEAR SUPPORTING STRUCTURE
Author(s): WARD GK; SHIHABELDEEN A; ZANNISHADJOPOULOS M; PRICE GB
Corporate Source: MCGILL UNIV,MCGILL CANC CTR,3655 DRUMMOND ST/MONTREAL H3G 1Y6/QUEBEC/CANADA/; MCGILL UNIV,MCGILL CANC CTR,3655 DRUMMOND ST/MONTREAL H3G 1Y6/QUEBEC/CANADA/
Journal: EXPERIMENTAL CELL RESEARCH, 1991, V195, N1, P92-98
Language: ENGLISH Document Type: ARTICLE

3/7/61 (Item 33 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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00993142 Genuine Article#: FM035 Number of References: 20
Title: THE BIME FAMILY OF BACTERIAL HIGHLY REPETITIVE SEQUENCES
Author(s): GILSON E; SAURIN W; PERRIN D; BACHELLIER S; HOFNUNG M
Corporate Source: INST PASTEUR,CNRS,UA 271,INSERM,U163,UNITE PROGRAMMAT MOLEC & TOXICOL GENET/F-75724 PARIS 15//FRANCE/
Journal: RESEARCH IN MICROBIOLOGY, 1991, V142, N2-3, P217-222
Language: ENGLISH Document Type: ARTICLE
Abstract: **Palindromic** units (PU or REP) were initially defined as a DNA sequence of 40 nucleotides which is highly repeated in the genome of several enterobacteria and found in clusters of up to six copies. It appears now that PU belong to a larger repeated DNA element, of up to 300 nucleotides, called BIME for bacterial interspersed mosaic element. BIME is a mosaic combination of ten small DNA motifs, including the PU sequence.

A central question concerning BIME is to determine whether they play a critical role within the cell. BIME exhibit only limited effects on local gene expression; it seems unlikely that these weak effects alone can account for the high BIME sequence homogeneity. It

has recently been shown that DNA **gyrase** and DNA polymerase I are able to specifically recognize BIME DNA in vitro. These findings suggest that BIME could play a role in the functional organization of the bacterial nucleoid. Hypotheses on their origin and evolution are discussed.

3/7/62 (Item 34 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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00718574 Genuine Article#: EQ479 Number of References: 60
Title: TRANSCRIPTION REGULATES OXOLINIC ACID-INDUCED DNA **GYRASE**
CLEAVAGE AT SPECIFIC SITES ON THE ESCHERICHIA-COLI CHROMOSOME
Author(s): CONDEMINE G; SMITH CL
Corporate Source: INST NATL SCI APPL, MICROBIOL LAB, BAT 406, 20 AVEALBERT
EINSTEIN/F-69621 VILLEURBANNE//FRANCE/; INST NATL SCI APPL, MICROBIOL
LAB, BAT 406, 20 AVEALBERT EINSTEIN/F-69621 VILLEURBANNE//FRANCE/; UNIV
CALIF BERKELEY LAWRENCE BERKELEY LAB, CTR HUMAN
GENOME/BERKELEY//CA/94720; UNIV CALIF BERKELEY, DEPT MOLEC & CELL
BIOL/BERKELEY//CA/94720
Journal: NUCLEIC ACIDS RESEARCH, 1990, V18, N24, P7389-7396
Language: ENGLISH Document Type: ARTICLE
Abstract: Prominent DNA **gyrase**-mediated cleavage sites, induced by
oxolinic acid, occur at specific, but infrequent, locations on the
Escherichia coli chromosome. These sites, which we call toposites, may
represent high affinity DNA **gyrase** binding sites or may mark
chromosomal regions that accumulate superhelical stress. Toposites are
usually grouped in 5 to 10 kb clusters that are mostly 50 to 100 kb
apart. The total number of clusters on the chromosome is between 50
and 100. The location of sites depends on the local sequence. The
extent of DNA **gyrase** cleavage at toposites can be strongly
modulated by transcription occurring at as far as 35 kb away.

3/7/63 (Item 1 from file: 50)
DIALOG(R) File 50:CAB Abstracts
(c) 2002 CAB International. All rts. reserv.

03100144 CAB Accession Number: 950108733
Somatic hypermutation.
Neuberger, M. S.; Milstein, C.
Medical Research Council Laboratory of Molecular Biology, Hills Road,
Cambridge CB2 2QH, UK.
Current Opinions in Immunology vol. 7 (2): p.248-254
Publication Year: 1995 --
Language: English
Document Type: Journal article
A review, focusing largely on mice and man. Somatic hypermutation in B
lymphocytes targets a domain around the rearranged V-region which, in the
kappa locus, extends from the leader V intron domain towards E kappa i/MAR
in the J-C intron. The mutations are largely nucleotide substitutions with
marked substitution preferences, in particular a bias towards transitions.
The hypermutation process exhibits strand discrimination as revealed by
nucleotide substitution preference. Hypermutation does not occur randomly
within the V-domain but exhibits favoured hotspots which are associated
with features of DNA primary (e.g. AGC/T) or secondary (e.g.
palindromic) structure. Full hypermutation of kappa transgenes

depends on the process of E kappa i/MAR and E kappa 3', but is not significantly affected by a promoter swap. The dependence of hypermutation on the presence of E kappa i/MAR with its associated cluster of binding sites for **topoisomerase** II suggests that E kappa i/MAR might play a role in the initiation of hypermutation by, for example, encouraging the formation of single-strand nicks. 69 ref.

3/7/64 (Item 1 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE
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00998899 1998245322
Comparative structural analysis by [sup 1H,sup 3sup 1P]-NMR and restrained molecular dynamics of two DNA hairpins from a strong DNA **topoisomerase** II cleavage site
Mauffret O.; Amir-Aslani A.; Maroun R.G.; Monnot M.; Lescot E.; Fermandjian S.
ADDRESS: S. Fermandjian, Dept Biol Structurale Pharmacol Mol, CNRS UMR 1772, PR2, Institut Gustave Roussy 94805, Villejuif Cedex, France
EMAIL: sfermand@igr.fr
Journal: Journal of Molecular Biology, 283/3 (643-655), 1998, United Kingdom
PUBLICATION DATE: October 30, 1998
CODEN: JMOBA
ISSN: 0022-2836
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 66

The structural analysis of two single-stranded DNAs d(AGCTTATCATCGATAAGCT) (ATC-19) and d(AGCTTATCGATGATAAGCT) (GAT-19) was performed by NMR and restrained molecular dynamics. These oligonucleotides reproduce the 15-33 segment of phage pBR322 DNA, which contains a strong cleavage site for **topoisomerase** II coupled to the antitumor drugs VP-16 and ellipticine. Because of their partial **palindromic** nature, the two oligonucleotides ATC-19 and GAT-19 may fold back into stable hairpin structures, consisting of a stem of eight base-pairs and a loop of three residues. NMR assignments and conformational parameters were determined from combined 2D NOESY, COSY and sup 1H-sup 3sup 1P spectra. Conformations of ATC-19 and GAT-19 hairpins were calculated using the X-PLOR 3.1 program. Structures were generated through simulated annealing procedures starting from 50 structures with randomized torsion angles. A good convergence was observed for ATC-19 molecules, while no consensus was found for GAT-19. Within the GAT-19 loop, the base stacking was poor and no hydrogen bond could be detected. In contrast, ATC-19 displayed a well-defined three residue loop stabilized by both extensive base stackings and hydrogen bonding between the N3 atom of the adenine ring and the amino group of the cytosine ring. The results confirm our earlier ATC-19 structure obtained by a completely different calculation procedure (JUMNA) and the higher thermal stability of ATC-19 compared to GAT-19. Moreover, due to its mismatched base-pair, the ATC-19 loop may be better described as a single residue loop rather than a three residue loop. Comparison of this loop to those containing sheared purine-purine base-pairs revealed striking resemblances, particularly on the backbone angle combination. Finally, the differences observed between the ATC-19 and GAT-19 structures could help toward understanding the sequential cleavage of DNA strands by **topoisomerase** II.

3/7/65 (Item 2 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE
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00012294 94013540
Specific interaction of IHF with RIBs, a class of bacterial repetitive DNA
elements located at the 3' end of transcription units
Boccard F.; Prentki P.
ADDRESS: F. Boccard, Department of Molecular Biology, University of Geneva,
1211 Geneva 4, Switzerland
Journal: EMBO Journal, 12/13 (5019-5027), 1993, United Kingdom
PUBLICATION DATE: 19930000
CODEN: EMJOD
ISSN: 0261-4189
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English

The prokaryotic REP (repetitive extragenic **palindromes**) or PU (**palindromic** units) sequences are often associated with other repetitive elements, forming arrangements which have been called 'BIMES' (bacterial interspersed mosaic elements). It is estimated that the Escherichia coli chromosome carries ~ 300-500 BIMES, whose biological role is at present unknown. We have identified a family of BIMES consisting of two converging REP sequences flanking a 35 bp conserved segment which carries a static DNA bend and a binding site for IHF, the integration host factor of E.coli. We estimate that the E.coli genome harbors ~ 100 copies of this module, which we name 'RIB' (reiterative ihf BIME). We have analyzed by gel retardation and by footprinting the in vitro interaction of IHF with individual RIBs, and shown that the protein binds strongly and specifically to their center. We have also demonstrated binding of IHF to the chromosomal population of RIBs, using a new approach which combines two-dimensional bandshift and Southern blotting. RIB elements are at the end of transcription units, and thus define a new class of ihf sites. Possible implications for genome structure and DNA topology are discussed.

3/7/66 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
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06619440 EMBASE No: 1996284219
Action of DNA **gyrase** at RIP elements in E. coli
Clarkson S.; Bates A.D.
Department of Biochemistry, University of Liverpool, PO Box 147, Liverpool
L69 3BX United Kingdom
Biochemical Society Transactions (BIOCHEM. SOC. TRANS.) (United Kingdom
) 1996, 24/3 (420S)
CODEN: BCSTB ISSN: 0300-5127
DOCUMENT TYPE: Journal; Conference Paper
LANGUAGE: ENGLISH

3/7/67 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

02355153 4460709

Comparative Structural Analysis by [H,P]-NMR and Restrained Molecular Dynamics of Two DNA Hairpins from a Strong DNA **Topoisomerase II** Cleavage Site

Mauffret, O.; Amir Aslani, A.; Maroun, R.G.; Monnot, M.; Lescot, E.; Fermandjian, S.

Department de Biologie Structurale et de Pharmacologie Moleculaire (CNRS UMR 1772), PR2, Institut Gustave Roussy, Villejuif Cedex, 94805, France
Journal of Molecular Biology vol. 283, no. 3, pp. 643-655 (1998)

ISSN: 0022-2836

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts 2: Nucleic Acids

The structural analysis of two single-stranded DNAs d(AGCTTATCATCGATAAGCT) (ATC-19) and d(AGCTTATCGATGATAAGCT) (GAT-19) was performed by NMR and restrained molecular dynamics. These oligonucleotides reproduce the 15-33 segment of phage pBR322 DNA, which contains a strong cleavage site for **topoisomerase II** coupled to the antitumor drugs VP-16 and ellipticine. Because of their partial **palindromic** nature, the two oligonucleotides ATC-19 and GAT-19 may fold back into stable hairpin structures, consisting of a stem of eight base-pairs and a loop of three residues. NMR assignments and conformational parameters were determined from combined 2D NOESY, COSY and super(1)H- super(31)P spectra. Conformations of ATC-19 and GAT-19 hairpins were calculated using the X-PLOR 3.1 program. Structures were generated through simulated annealing procedures starting from 50 structures with randomized torsion angles. A good convergence was observed for ATC-19 molecules, while no consensus was found for GAT-19. Within the GAT-19 loop, the base stacking was poor and no hydrogen bond could be detected. In contrast, ATC-19 displayed a well-defined three residue loop stabilized by both extensive base stackings and hydrogen bonding between the N3 atom of the adenine ring and the amino group of the cytosine ring. The results confirm our earlier ATC-19 structure obtained by a completely different calculation procedure (JUMNA) and the higher thermal stability of ATC-19 compared to GAT-19. Moreover, due to its mismatched base-pair, the ATC-19 loop may be better described as a single residue loop rather than a three residue loop. Comparison of this loop to those containing sheared purine times purine base-pairs revealed striking resemblances, particularly on the backbone angle combination. Finally, the differences observed between the ATC-19 and GAT-19 structures could help toward understanding the sequential cleavage of DNA strands by **topoisomerase II**.

3/7/68 (Item 2 from file: 76)

DIALOG(R)File 76:Life Sciences Collection

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00549888 0238419

Recognition Sites of Eukaryotic DNA **Topoisomerase I**: DNA Nucleotide Sequencing Analysis of Topo I Cleavage Sites on SV40 DNA.

Liu, L.F.; Edwards, K.A.; Halligan, B.D.; Davis, J.L.; Nivera, N.L.
Dep. Physiol. Chem., Johns Hopkins Med. Sch., Baltimore, MD 21205, USA
NUCLEIC ACIDS RES. vol. 10, no. 8, pp. 2565-2576 (1982.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts Part 2: Nucleic Acids; Genetics Abstracts

Eukaryotic DNA **topoisomerase I** introduces transient single-stranded breaks on double-stranded DNA and spontaneously breaks down

single-stranded DNA. Consistent with other reports, the eukaryotic enzymes, in contrast to prokaryotic type I topoisomerases, links to the 3'-end of the cleaved DNA and generates a free 5'-hydroxyl end on the other half of the broken DNA strand. From 287 nucleotides sequenced, 68 cleavage sites were mapped. The majority of the cleavage sites were present on both double and single-stranded DNA at exactly the same nucleotide positions, suggesting that the DNA sequence is essential for enzyme recognition. There is a high probability to exclude G from positions -4, -2, -1, and +1, T from position -3, and A from position -1. These five positions (-4 to +1 oriented in the 5' to 3' direction) around the cleavage sites must interact intimately with topo I and thus are essential for enzyme recognition. One topo I cleavage site which shows an atypical cleavage sequence maps in the middle of a **palindromic** sequence near the origin of SV40 DNA replication. It occurs only on single-stranded SV40 DNA, suggesting that the DNA hairpin can alter the cleavage specificity. The strongest cleavage site maps near the origin of SV40 DNA replication at nucleotide 31-32 and has a pentanucleotide sequence of 5'-TGACT-3'.